



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/229,751B  
Source: 1600  
Date Processed by STIC: 7/22/2003

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/229,757B
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 Misaligned Amino Numbering	The numbering under each 3 <sup>rd</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.	
11 Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	



1600

## RAW SEQUENCE LISTING

DATE: 07/22/2003

PATENT APPLICATION: US/09/229,751B

TIME: 13:49:33

Input Set : A:\Dosseq.715

Output Set: N:\CRF4\07222003\I229751B.raw

## SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Turnbough, Charles K

8 (ii) TITLE OF INVENTION: PEPTIDE LIGANDS THAT BIND TO SURFACES

9 OF

10 BACTERIAL CELLS

E--> 12 (iii) NUMBER OF SEQUENCES: 2682 (see p. 8)

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Glenna Hendricks

16 (B) STREET: P.O. Box 2509

17 (C) CITY: Fairfax

18 (D) STATE: VA

19 (E) COUNTRY: USA

20 (F) ZIP: 22031

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

28 (vi) CURRENT APPLICATION DATA:

29 (A) APPLICATION NUMBER: US/09/229,751B

30 (B) FILING DATE: 14-Jan-1999

31 (C) CLASSIFICATION:

33 (viii) ATTORNEY/AGENT INFORMATION:

34 (A) NAME: Hendricks, Glenna M

35 (B) REGISTRATION NUMBER: 32,535

36 (C) REFERENCE/DOCKET NUMBER: turn

38 (ix) TELECOMMUNICATION INFORMATION:

39 (A) TELEPHONE: (703) 425-8405

40 (B) TELEFAX: (703) 425-8406

Does Not Comply  
Corrected Diskette Needed

pp 1-8

## ERRORED SEQUENCES

64 (2) INFORMATION FOR SEQ ID NO: 2:

66 (i) SEQUENCE CHARACTERISTICS:

67 (A) LENGTH: 21 base pairs

68 (B) TYPE: nucleic acid

69 (C) STRANDEDNESS: single

70 (D) TOPOLOGY: unknown

72 (ii) MOLECULE TYPE: DNA (genomic)

74 (iii) HYPOTHETICAL: NO

76 (iv) ANTI-SENSE: NO

p. 2 (global error)

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Input Set : A:\Dosseq.715

Output Set: N:\CRF4\07222003\I229751B.raw

80 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

E--> 82 AATCATTTTT TGATTAAGCC G

W--> 83 21

85 (2) INFORMATION FOR SEQ ID NO: 3:

87 (i) SEQUENCE CHARACTERISTICS:

88 (A) LENGTH: 21 base pairs

89 (B) TYPE: nucleic acid

90 (C) STRANDEDNESS: single

91 (D) TOPOLOGY: unknown

93 (ii) MOLECULE TYPE: DNA (genomic)

95 (iii) HYPOTHETICAL: NO

97 (iv) ANTI-SENSE: NO

101 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

E--> 103 AATCATTTTT TGAGGTCTCC G

W--> 104 21

127 (2) INFORMATION FOR SEQ ID NO: 5:

129 (i) SEQUENCE CHARACTERISTICS:

130 (A) LENGTH: 21 base pairs

131 (B) TYPE: nucleic acid

132 (C) STRANDEDNESS: single

133 (D) TOPOLOGY: unknown

135 (ii) MOLECULE TYPE: DNA (genomic)

137 (iii) HYPOTHETICAL: NO

139 (iv) ANTI-SENSE: NO

143 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

E--> 145 AATCATTTTC TTCCTAAGGT G

W--> 146 21

148 (2) INFORMATION FOR SEQ ID NO: 6:

150 (i) SEQUENCE CHARACTERISTICS:

151 (A) LENGTH: 21 base pairs

152 (B) TYPE: nucleic acid

153 (C) STRANDEDNESS: single

154 (D) TOPOLOGY: unknown

156 (ii) MOLECULE TYPE: DNA (genomic)

158 (iii) HYPOTHETICAL: NO

160 (iv) ANTI-SENSE: NO

164 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

E--> 166 AATCATTTTC TGTGCGGCC G

W--> 167 21

169 (2) INFORMATION FOR SEQ ID NO: 7:

171 (i) SEQUENCE CHARACTERISTICS:

172 (A) LENGTH: 21 base pairs

173 (B) TYPE: nucleic acid

174 (C) STRANDEDNESS: single

175 (D) TOPOLOGY: unknown

177 (ii) MOLECULE TYPE: peptide

179 (iii) HYPOTHETICAL: NO

181 (iv) ANTI-SENSE: NO

185 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

*see item 1 on Error Summary Sheet*

*same error*

*same*

*same*

*? This is a DNA sequence.*

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Input Set : A:\Dosseq.715

Output Set: N:\CRF4\07222003\I229751B.raw

E--&gt; 187 AATCATTTTC TGCCTCGTTG G

W--&gt; 188 21

190 (2) INFORMATION FOR SEQ ID NO: 8:

192 (i) SEQUENCE CHARACTERISTICS:

193 (A) LENGTH: 21 base pairs

194 (B) TYPE: nucleic acid

195 (C) STRANDEDNESS: single

196 (D) TOPOLOGY: unknown

198 (ii) MOLECULE TYPE: peptide?

200 (iii) HYPOTHETICAL: NO

202 (iv) ANTI-SENSE: NO

206 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

E--&gt; 208 AATCATTTTT TGCCTCCTCG G

W--&gt; 209 21

211 (2) INFORMATION FOR SEQ ID NO: 9:

213 (i) SEQUENCE CHARACTERISTICS:

214 (A) LENGTH: 21 base pairs

215 (B) TYPE: nucleic acid

216 (C) STRANDEDNESS: single

217 (D) TOPOLOGY: unknown

219 (ii) MOLECULE TYPE: DNA (genomic)

221 (iii) HYPOTHETICAL: NO

223 (iv) ANTI-SENSE: NO

227 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

E--&gt; 229 AATCATTTTC TGATGCCGAA G

W--&gt; 230 21

232 (2) INFORMATION FOR SEQ ID NO: 10:

234 (i) SEQUENCE CHARACTERISTICS:

235 (A) LENGTH: 21 base pairs

236 (B) TYPE: nucleic acid

237 (C) STRANDEDNESS: single

238 (D) TOPOLOGY: unknown

240 (ii) MOLECULE TYPE: DNA (genomic)

242 (iii) HYPOTHETICAL: NO

244 (iv) ANTI-SENSE: NO

248 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

E--&gt; 250 AATCATTTTC TGCCTACTGG G

W--&gt; 251 21

253 (2) INFORMATION FOR SEQ ID NO: 11:

255 (i) SEQUENCE CHARACTERISTICS:

256 (A) LENGTH: 21 base pairs

257 (B) TYPE: nucleic acid

258 (C) STRANDEDNESS: single

259 (D) TOPOLOGY: unknown

261 (ii) MOLECULE TYPE: DNA (genomic)

263 (iii) HYPOTHETICAL: NO

265 (iv) ANTI-SENSE: NO

269 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

E--&gt; 271 AATCATTTTC TTAAGGGGAC G

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/229,751B

DATE: 07/22/2003

TIME: 13:49:33

Input Set : A:\Dosseq.715

Output Set: N:\CRF4\07222003\I229751B.raw

W--> 272 21  
274 (2) INFORMATION FOR SEQ ID NO: 12:  
276 (i) SEQUENCE CHARACTERISTICS:  
277 (A) LENGTH: 21 base pairs  
278 (B) TYPE: nucleic acid  
279 (C) STRANDEDNESS: single  
280 (D) TOPOLOGY: unknown  
282 (ii) MOLECULE TYPE: DNA (genomic)  
284 (iii) HYPOTHETICAL: NO  
286 (iv) ANTI-SENSE: NO  
290 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

E--&gt; 292 ATTCATTTTC TTCTTTGGCG T

W--> 293 21  
295 (2) INFORMATION FOR SEQ ID NO: 13:  
297 (i) SEQUENCE CHARACTERISTICS:  
298 (A) LENGTH: 21 base pairs  
299 (B) TYPE: nucleic acid  
300 (C) STRANDEDNESS: single  
301 (D) TOPOLOGY: unknown  
303 (ii) MOLECULE TYPE: DNA (genomic)  
305 (iii) HYPOTHETICAL: NO  
307 (iv) ANTI-SENSE: NO  
311 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

E--&gt; 313 AATCATTTTC TGATTAGGAA G

W--> 314 21  
316 (2) INFORMATION FOR SEQ ID NO: 14:  
318 (i) SEQUENCE CHARACTERISTICS:  
319 (A) LENGTH: 21 base pairs  
320 (B) TYPE: nucleic acid  
321 (C) STRANDEDNESS: single  
322 (D) TOPOLOGY: unknown  
324 (ii) MOLECULE TYPE: DNA (genomic)  
326 (iii) HYPOTHETICAL: NO  
328 (iv) ANTI-SENSE: NO  
332 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

E--&gt; 334 AATCATTTTC TGCCGACTGC T

W--> 335 21  
379 (2) INFORMATION FOR SEQ ID NO: 17:  
381 (i) SEQUENCE CHARACTERISTICS:  
382 (A) LENGTH: 21 base pairs  
383 (B) TYPE: nucleic acid  
384 (C) STRANDEDNESS: single  
385 (D) TOPOLOGY: unknown  
387 (ii) MOLECULE TYPE: DNA (genomic)  
389 (iii) HYPOTHETICAL: NO  
391 (iv) ANTI-SENSE: NO  
395 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

E--&gt; 397 ATTCATTTTT TGCCGCAGAA T

W--&gt; 398 21

## RAW SEQUENCE LISTING

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TIME: 13:49:33

Input Set : A:\Dosseq.715

Output Set: N:\CRF4\07222003\I229751B.raw

926 (2) INFORMATION FOR SEQ ID NO: 43:  
 928 (i) SEQUENCE CHARACTERISTICS:  
 929 (A) LENGTH: 7 amino acids  
 930 (B) TYPE: amino acid  
 931 (C) STRANDEDNESS: single  
 932 (D) TOPOLOGY: unknown  
 934 (ii) MOLECULE TYPE: peptide  
 936 (iii) HYPOTHETICAL: NO  
 938 (iv) ANTI-SENSE: NO  
 942 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
 E--> 944 ~~Thr-Tyr-Pro-Val-Pro-His-Arg~~  
 E--> 945 1 5

989 (2) INFORMATION FOR SEQ ID NO: 46:  
 991 (i) SEQUENCE CHARACTERISTICS:  
 992 (A) LENGTH: 21 base pairs  
 993 (B) TYPE: nucleic acid  
 994 (C) STRANDEDNESS: single  
 995 (D) TOPOLOGY: unknown  
 997 (ii) MOLECULE TYPE: DNA (genomic)  
 999 (iii) HYPOTHETICAL: NO  
 1001 (iv) ANTI-SENSE: NO  
 1005 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

E--> 1007 ACGCATCGTT TGCCTTCTCG G  
 W--> 1008 21

1010 (2) INFORMATION FOR SEQ ID NO: 47:  
 1012 (i) SEQUENCE CHARACTERISTICS:  
 1013 (A) LENGTH: 21 base pairs  
 1014 (B) TYPE: nucleic acid  
 1015 (C) STRANDEDNESS: single  
 1016 (D) TOPOLOGY: unknown  
 1018 (ii) MOLECULE TYPE: DNA (genomic)  
 1020 (iii) HYPOTHETICAL: NO  
 1022 (iv) ANTI-SENSE: NO  
 1026 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

E--> 1028 GTTACTAGTA GGGGAATGT T  
 W--> 1029 21

1031 (2) INFORMATION FOR SEQ ID NO: 48:  
 1033 (i) SEQUENCE CHARACTERISTICS:  
 1034 (A) LENGTH: 21 base pairs  
 1035 (B) TYPE: nucleic acid  
 1036 (C) STRANDEDNESS: single  
 1037 (D) TOPOLOGY: unknown  
 1039 (ii) MOLECULE TYPE: DNA (genomic)  
 1041 (iii) HYPOTHETICAL: NO  
 1043 (iv) ANTI-SENSE: NO  
 1047 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

E--> 1049 AAGCTGTGGG TGATTCTCA G  
 W--> 1050 21

1052 (2) INFORMATION FOR SEQ ID NO: 49:

*delete all dashes - they are invalid  
 do not use TAB codes  
 between amino acid  
 numbers  
 use space character*

*see item 1 on Error Summary sheet*

*same*

*same*

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Input Set : A:\Dosseq.715

Output Set: N:\CRF4\07222003\I229751B.raw

1054 (i) SEQUENCE CHARACTERISTICS:  
1055 (A) LENGTH: 21 base pairs  
1056 (B) TYPE: nucleic acid  
1057 (C) STRANDEDNESS: single  
1058 (D) TOPOLOGY: unknown  
1060 (ii) MOLECULE TYPE: DNA (genomic)  
1062 (iii) HYPOTHETICAL: NO  
1064 (iv) ANTI-SENSE: NO  
1068 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:  
E--> 1070 TATTCGCCTC CTCATAGGCA T *same*  
W--> 1071 21  
1220 (2) INFORMATION FOR SEQ ID NO: 57:  
1222 (i) SEQUENCE CHARACTERISTICS:  
1223 (A) LENGTH: 21 base pairs  
1224 (B) TYPE: nucleic acid  
1225 (C) STRANDEDNESS: single  
1226 (D) TOPOLOGY: unknown  
1228 (ii) MOLECULE TYPE: DNA (genomic)  
1230 (iii) HYPOTHETICAL: NO  
1232 (iv) ANTI-SENSE: NO  
1236 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
E--> 1238 TCGTATCCTC CGTATTTTGA T *same*  
W--> 1239 21  
1241 (2) INFORMATION FOR SEQ ID NO: 58:  
1243 (i) SEQUENCE CHARACTERISTICS:  
1244 (A) LENGTH: 21 base pairs  
1245 (B) TYPE: nucleic acid  
1246 (C) STRANDEDNESS: single  
1247 (D) TOPOLOGY: unknown  
1249 (ii) MOLECULE TYPE: DNA (genomic)  
1251 (iii) HYPOTHETICAL: NO  
1253 (iv) ANTI-SENSE: NO  
1257 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:  
E--> 1259 CTTTTGTGCG CTCTGCATCG T *same*  
W--> 1260 21  
1262 (2) INFORMATION FOR SEQ ID NO: 59:  
1264 (i) SEQUENCE CHARACTERISTICS:  
1265 (A) LENGTH: 21 base pairs  
1266 (B) TYPE: nucleic acid  
1267 (C) STRANDEDNESS: single  
1268 (D) TOPOLOGY: unknown  
1270 (ii) MOLECULE TYPE: DNA (genomic)  
1272 (iii) HYPOTHETICAL: NO  
1274 (iv) ANTI-SENSE: NO  
1278 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
E--> 1280 TTTGATTCTC CGCTTCGTCG G *same*  
W--> 1281 21  
1662 (2) INFORMATION FOR SEQ ID NO: 78:  
1664 (i) SEQUENCE CHARACTERISTICS:



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Input Set : A:\Dosseq.715

Output Set: N:\CRF4\07222003\I229751B.raw

1665 (A) LENGTH: 7 amino acids  
1666 (B) TYPE: amino acid  
1667 (C) STRANDEDNESS: single  
1668 (D) TOPOLOGY: unknown  
1670 (ii) MOLECULE TYPE: peptide  
1672 (iii) HYPOTHETICAL: NO  
1674 (iv) ANTI-SENSE: NO  
1678 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:  
1680 Phe Asp Ser Pro Leu Arg Arg  
1681 1 5  
1683 (2) INFORMATION FOR SEQ ID NO: 78:  
1685 (i) SEQUENCE CHARACTERISTICS:  
1686 (A) LENGTH: 7 amino acids  
1687 (B) TYPE: amino acid  
1688 (C) STRANDEDNESS: single  
1689 (D) TOPOLOGY: unknown  
1691 (ii) MOLECULE TYPE: peptide  
1693 (iii) HYPOTHETICAL: NO  
1695 (iv) ANTI-SENSE: NO  
1699 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:  
1701 Trp Ser Pro Leu His Lys His  
1702 1 5

OK  
See P. 8

## (2) INFORMATION FOR SEQ ID NO: 82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Ser Pro Leu Xaa Xaa His

1

5

last sequence in submitted  
file